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1	CAG	AGG	TTG	CCC	CGG	ATG	CAG	GAG	GAT	TCC	CCC	TTG	GAG	GAG	GCT
16	Leu	Leu	Gly	Iys	Met	Thr	His	Trp	Ala	Arg	Arg	Ile	Cys	Pro	Val
46	CTT	CTG	GGG	AAG	ATG	ACC	CAC	TGG	GCG	AGG	AGG	ATC	TGC	CCA	GTG
31	Lys	Arg	Ile	His	Pro	Glu	Arg	Arg	Ile	His	Pro	Glu	Arg	Arg	Ile
91	AAG	AGG	ATT	CAC	CCA	GAG	AGG	AGG	ATC	CAC	CCG	GAG	AGG	AGG	ATC
46	Tyr	Leu	Glu	Arg	Arg	Ile	Tyr	Leu	Glu	Arg	Arg	Ile	Tyr	Leu	Lys
136	TAC	CTG	GAG	AGG	AGG	ATC	TAC	CTG	GAG	AGG	AGG	ATC	TAC	CTG	AAG
61	Leu	Met	Pro	Lys	Ser	Glu	Glu	Glu	Gly	Ser	Leu	Lys	Leu	Glu	Asp
181	TTA	ATG	CCT	AAA	TCA	GAA	GAA	GAG	GGC	TCC	CTG	AAG	TTA	GAG	GAT
76	Leu	Pro	Thr	Val	Glu	Ala	Pro	Gly	Asp	Pro	Gln	Glu	Pro	Gln	Asn
226	CTA	CCT	ACT	GTT	GAG	GCT	CCT	GGA	GAT	CCT	CAA	GAA	CCC	CAG	AAT
91	Asn	Ala	His	Arg	Asp	Lys	Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg
271	AAT	GCC	CAC	AGG	GAC	AAA	GAA	GGG	GAT	GAC	CAG	AGT	CAT	TGG	CGC
106	Tyr	Gly	Gly	Asp	Pro	Pro	Gly	Pro	Gly	Cys	Pro	Gln	Pro	Ala	Arg
316	TAT	GGA	GGC	GAC	CCG	CCT	GGC	CCC	GGG	TGT	CCC	CAG	CCT	GCG	CGG
121	Ala	Ala	Ser	Ser	Pro	Arg	Trp	Ile	Ser	Ala	Pro	Ser	Ser	Pro	Pro
361	GCC	GCT	TCC	AGT	CCC	CGG	TGG	ATA	TCC	GCC	CCC	AGC	TCG	CCG	CCT
136	Ser	Ala	Arg	Pro	Cys	Ala	Pro	Trp	Asn	Ser	Trp	Ala	Ser	Ser	Ser
406	TCT	GCC	CGG	CCC	TGC	GCC	CCC	TGG	AAC	TCC	TGG	GCT	TCC	AGC	TCC
151	Arg	Arg	Ser	Gln	Asn	Cys	Ala	Cys	Arg	Gln	Trp	Pro	Gln	Cys	Ala
451	CGC	CGC	TCC	CAG	AAC	TGC	GCC	TGC	AGA	CAA	TGG	CCA	CAG	TGT	GCA
166	Thr	Asp	Pro	Ala	Ser	Trp	Ala	Arg	Asp	Gly	Ser	Gly	Ser	Arg	Ala
496	ACT	GAC	CCT	GCC	TCC	TGG	GCT	AGA	GAT	GGC	TCT	GGG	TCC	CGG	GCG
181	Gly	Val	Pro	Ala	Leu	Gln	Leu	His	Leu	His	Trp	Gly	Ala	Ala	Gly
541	GGA	GTA	CCG	GCT	CTG	CAG	CTG	CAT	CTG	CAC	TGG	GGG	GCT	GCA	GGT
196	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	Phe	Pro	Ala
586	CGT	CCG	GGC	TCG	GAG	CAC	ACT	GTG	GAA	GGC	CAC	CGT	TTC	CCT	GCC
211	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	Val	Asp
631	GAG	ATC	CAC	GTG	GTT	CAC	CTC	AGC	ACC	GCC	TTT	GCC	AGA	GTT	GAC
226	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Pro	Phe
676	GAG	GCC	TTG	GGG	CGC	CCG	GGA	GGC	CTG	GCC	GTG	TTG	GCG	CCT	TTC

FIG. 1 A

241	Trp	Arg	Arg	Ala	Arg	Lys	Lys	Thr	Val	Ser	Tyr	Glu	Gln	Leu	Leu
721	TGG	AGG	AGG	GCC	CGG	AAG	AAA	ACA	GTG	TCC	TAT	GAG	CAG	TTG	CTG
256	Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val
766	TCT	CGC	TTG	GAA	GAA	ATC	GCT	GAG	GAA	GGC	TCA	GAG	ACT	CAG	GTC
271	Pro	Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	Ser	Arg
811	CCA	GGA	CTG	GAC	ATA	TCT	GCA	CTC	CTG	CCC	TCT	GAC	TTC	AGC	CGC
286	Tyr	Phe	Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	Gln
856	TAC	TTC	CAA	TAT	GAG	GGG	TCT	CTG	ACT	ACA	CCG	CCC	TGT	GCC	CAG
301	Gly	Val	Ile	Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala
901	GGT	GTC	ATC	TGG	ACT	GTG	TTT	AAC	CAG	ACA	GTG	ATG	CTG	AGT	GCT
316	Lys	Gln	Leu	His	Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp
946	AAG	CAG	CTC	CAC	ACC	CTC	TCT	GAC	ACC	CTG	TGG	GGA	CCT	GGT	GAC
331	Ser	Arg	Leu	Gln	Leu	Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly
991	TCT	CGG	CTA	CAG	CTG	AAC	TTC	CSA	GCG	ACG	CAG	CCT	TTG	AAT	GGG
346	Arg	Val	Ile	Glu	Ala	Ser	Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro
1036	CGA	GTG	ATT	GAG	GCC	TCC	TTC	CCT	GCT	GGA	GTG	GAC	AGC	AGT	CCT
361	Arg	Ala	Ala	Glu	Pro	Val	Gln	Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly
1081	CGG	GCT	GCT	GAG	CCA	GTC	CAG	CTG	AAT	TCC	TGC	CTG	GCT	GCT	GGT
376	Asp	Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser
1126	GAC	ATC	CTA	GCC	CTG	GTT	TTT	GGC	CTC	CTT	TTT	GCT	GTC	ACC	AGC
391	Val	Ala	Phe	Leu	Val	Gln	Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr
1171	GTC	GCG	TTC	CTT	GTG	CAG	ATG	AGA	AGG	CAG	CAC	AGA	AGG	GGA	ACC
406	Lys	Gly	Gly	Val	Ser	Val	Pro	Pro	Ser	Arg	Gly	Ser	Arg	Asp	Trp
1216	AAA	GGG	GGT	GTG	AGC	GTA	CCG	CCC	AGC	AGA	GGT	AGC	CGA	GAC	TGG
421	Ser	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Met	***					
1261	AGC	CTA	GAG	GCT	GGA	TCT	TGG	AGA	ATG	TGA	GAA	GCC	AGC	CAG	AGG
1306	CAT	CTG	AGG	GGG	AGC	CGG	TAA	CTG	TCC	TGT	CCT	GCT	CAT	TAT	GCC
1351	ACT	TCC	TTT	TAA	CTG	CCA	AGA	AAT	TTT	TTA	AAA	TAA	ATA	TTT	ATA
1396	AT														

FIG. 1 B

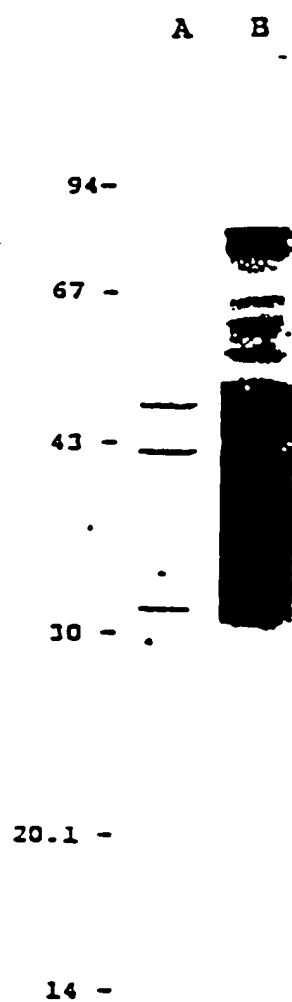


FIG. 2

A B C D

58K -

54K -



FIG. 3

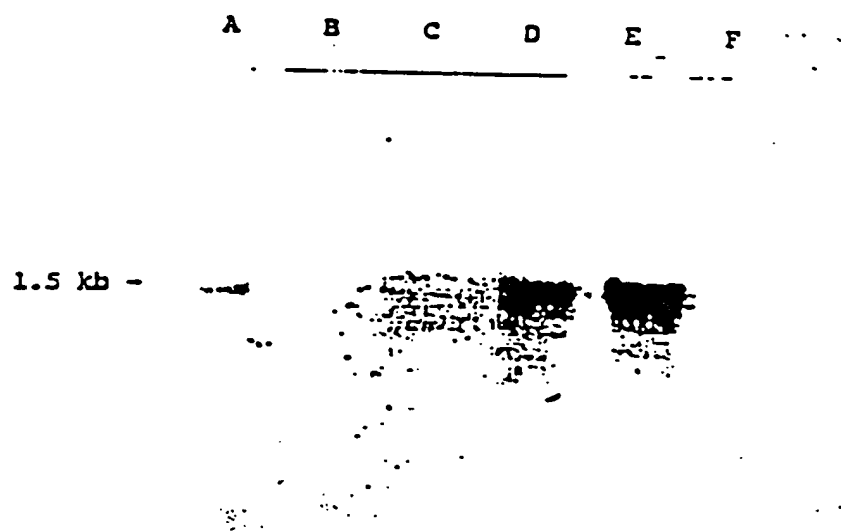


FIG. 4

*Pst*I

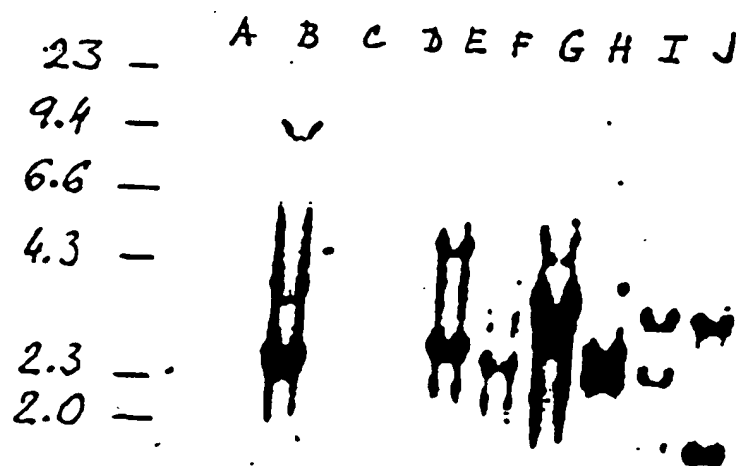


FIG. 5

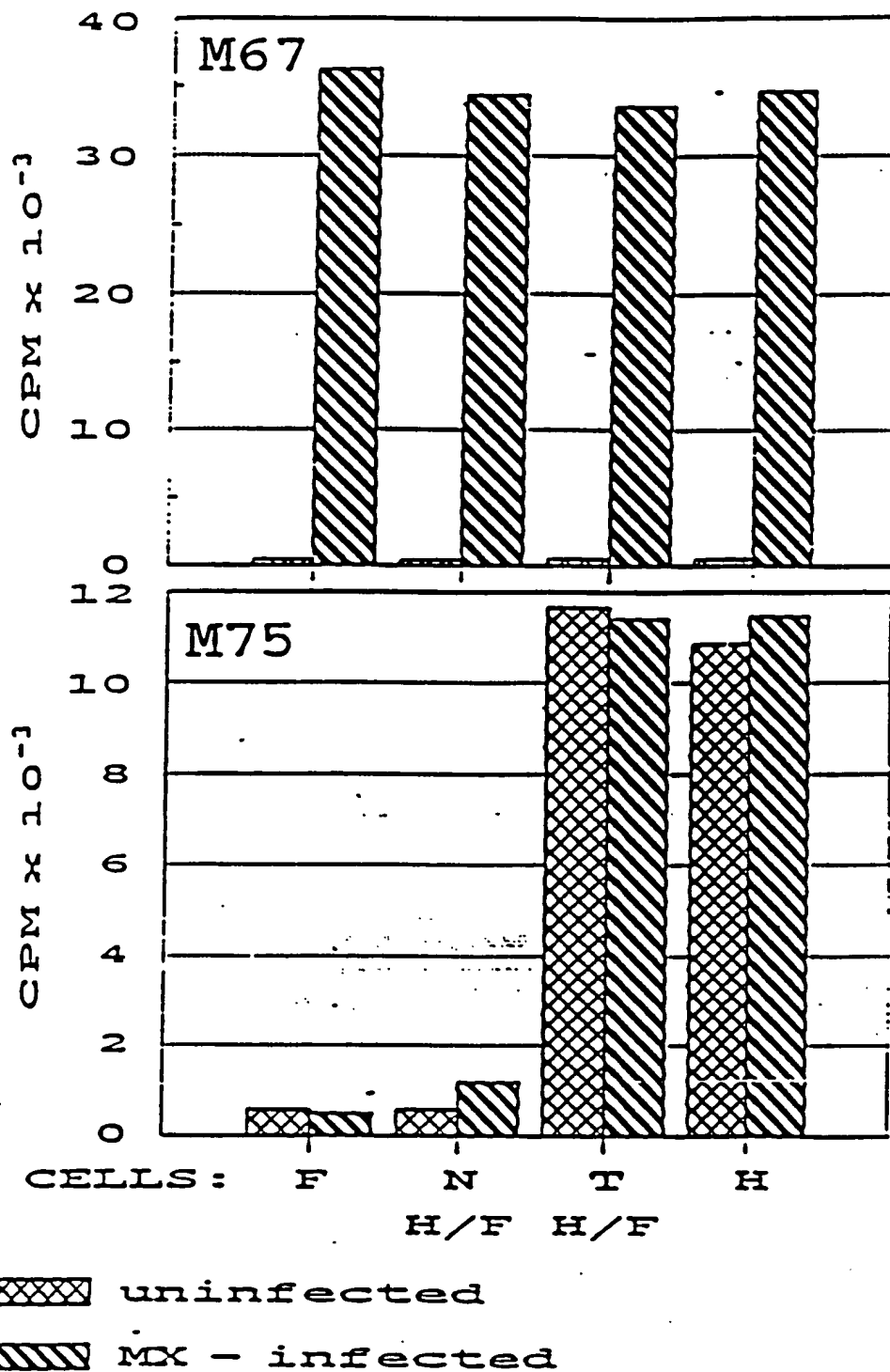


FIG. 6



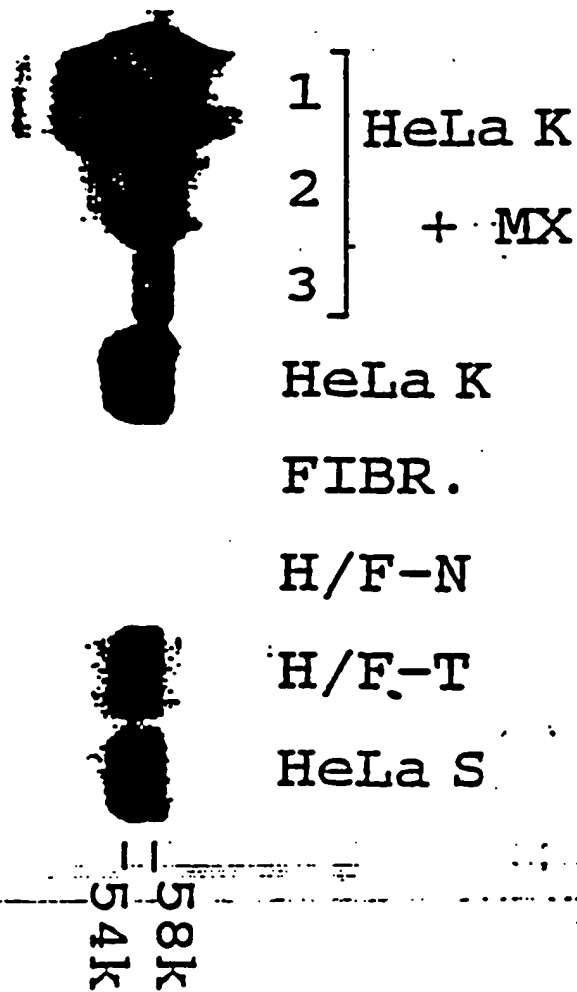


FIG. 7

+ ME

0 ME

A B C D E F

A B C D E F

153k—

58k—

54k—

FIG. 8

A B C D E F G H I J K L M N O P

58k

54k

FIG. 9

+ME OME

A B A B

153k-

58k-

54k-

FIG. 10

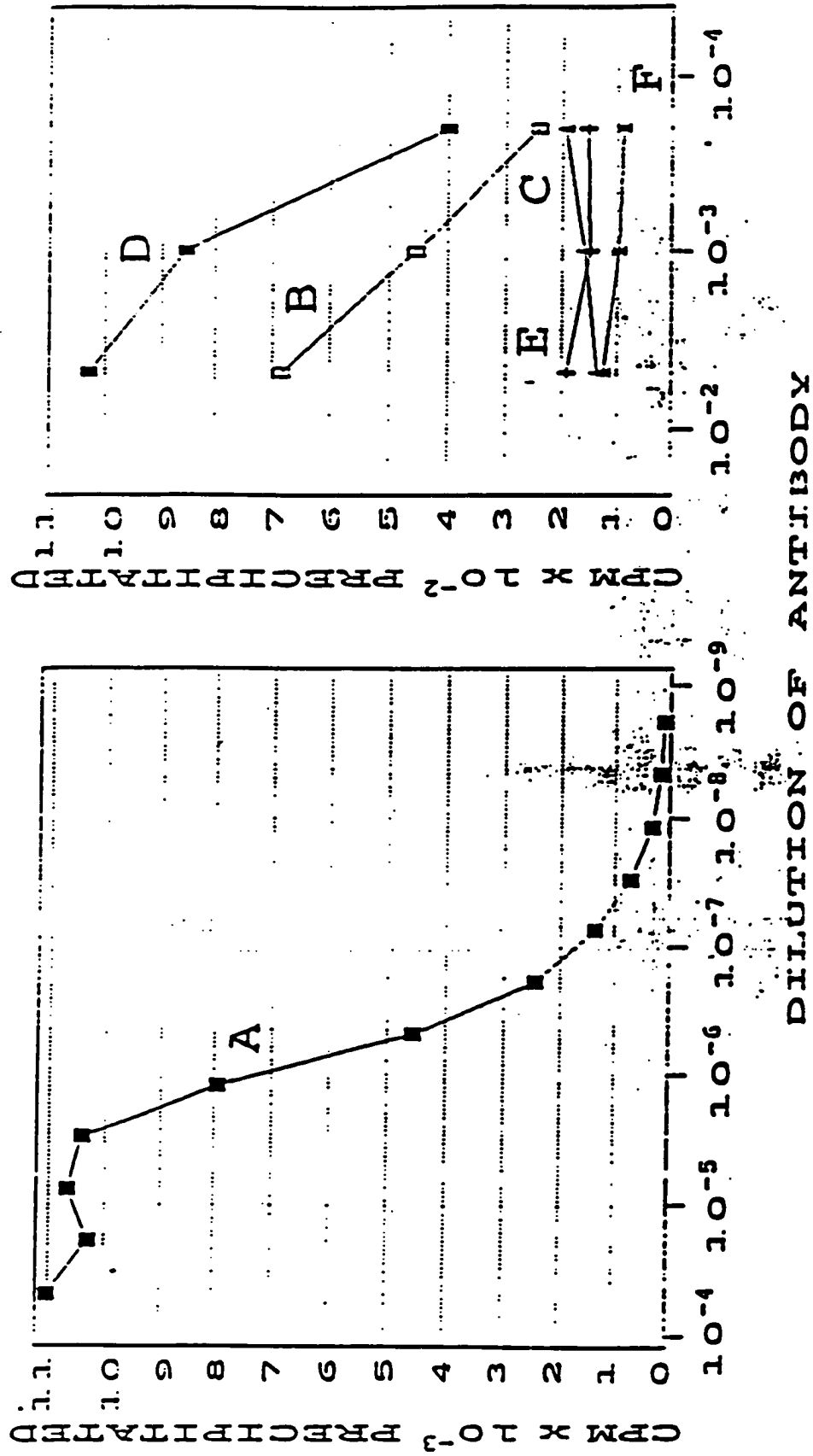


FIG. 11

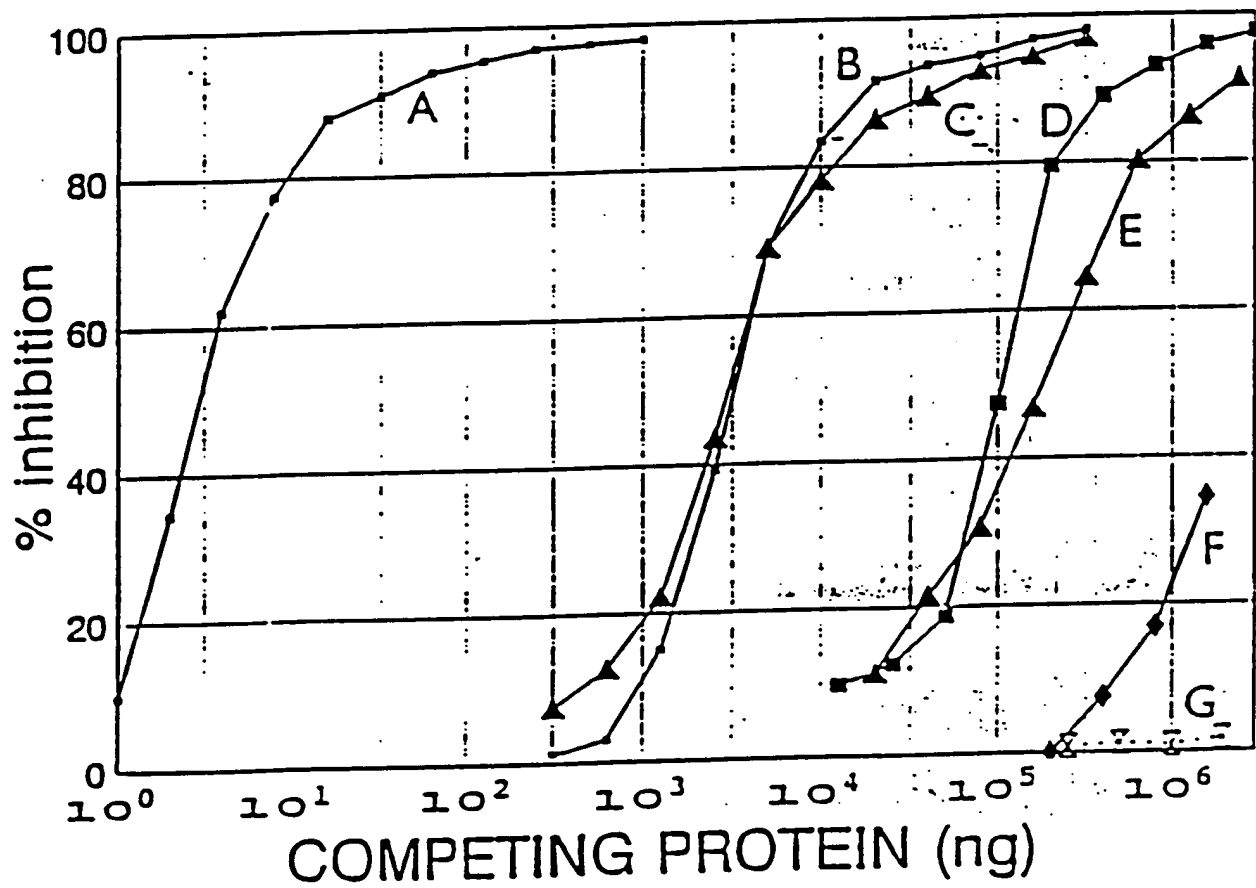
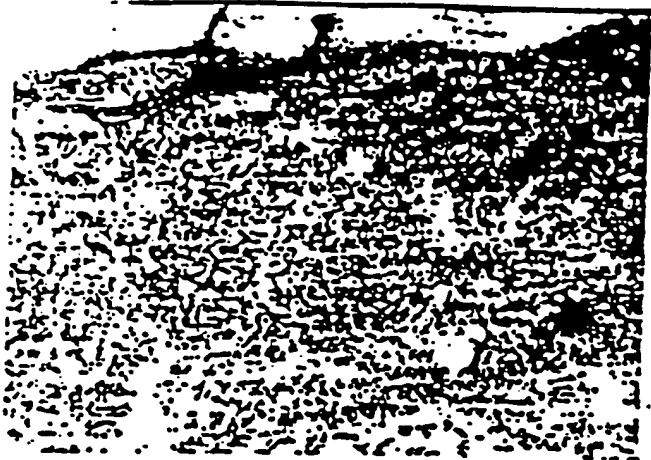
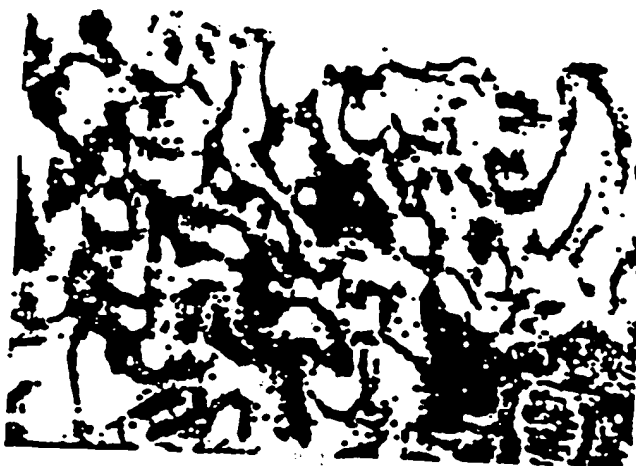


FIG. 12

A



B



C



D



E

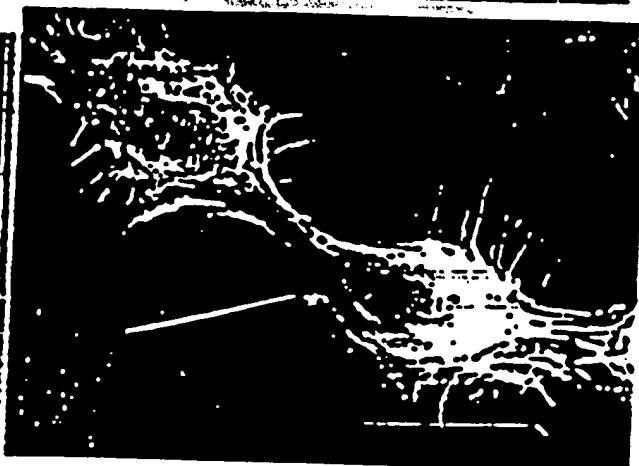


FIG. 13

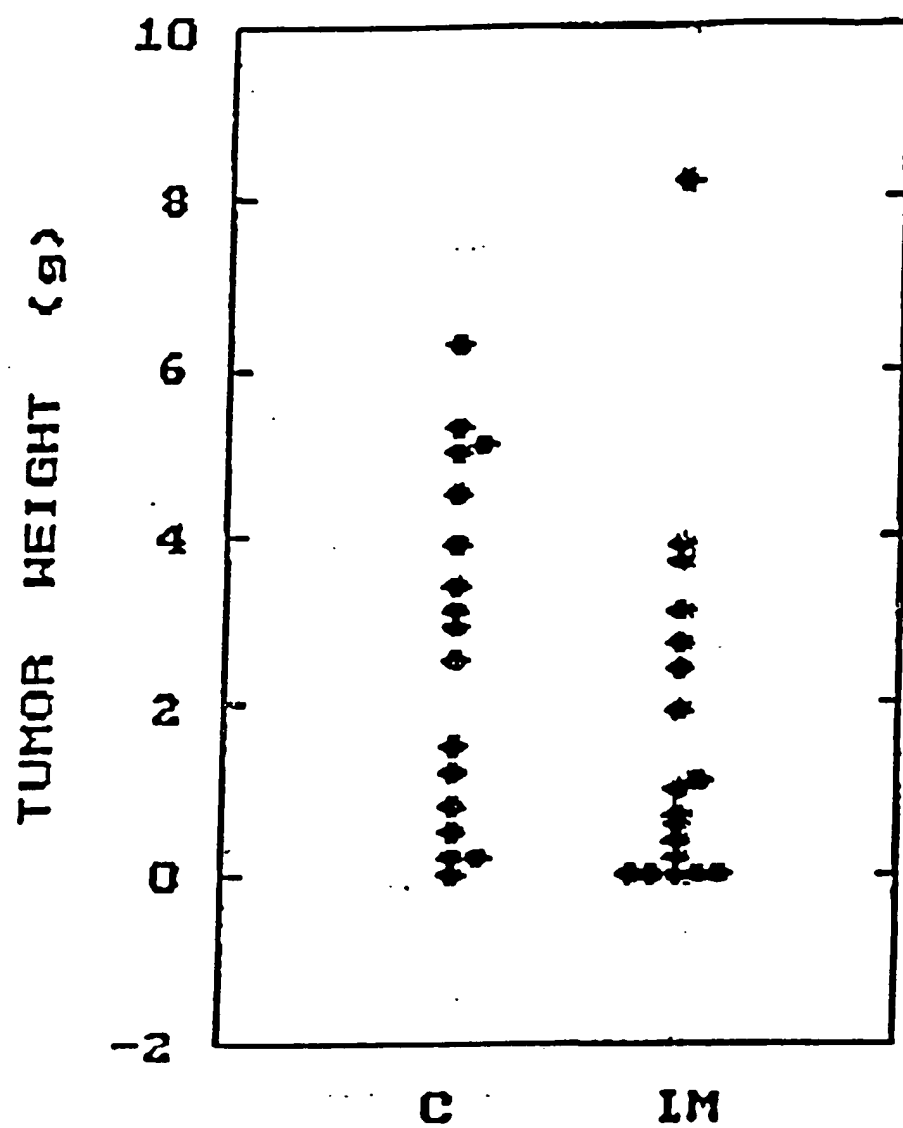


FIG. 14



```

1          N A P L C P S P V L P L L F P A      16
1 ACAGTCAGGCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGTGATCCCCGGCC      60

17 P A P G L T V Q L L L S L L L L N P V H      36
61 CTGCTCCAGGCGCTCACTGTGCAACTGCTGCTGTGCTGCTGCTTCTGTATGCTGTGCTATC      120

37 P Q R L P R N Q E D S P L E E A L L G K      56
121 CCCAGAGGTGCCCCGGATGCAGGAGGATTCCTCCCTTGGAGGAGGCTCTTCTGGGGAAGA      180

57 H T H W A R R I C P V K R I H P E R R I      76
181 TGACCCACTGGGCGAGGAGGATCTGCCAGTGAACAGGATTACCCAGAGAGGAGGATCC      240

77 H P E R R I Y L E R R I Y L E R R I Y L      96
241 ACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGA      300

97 K L N P K S E E E G S L K L E D L P T V      116
301 AGTTAATGCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTG      360

117 E A P G D P Q E P Q N N A H R D K E G D      136
361 AGGCTCCTGGAGATCCTCAAGAACCCCAAGATATCCCAAGGACCAAGAGAGGAGGATG      420

137 D Q S H W R Y G C D P F G F G C P Q P A      156
421 ACCAGAGTCATTGCGCTATGGAGCGGAGCCGCGCTGGCGCGCGGTGTCCCGAGCCTCCGC      480

157 R A A S S P R W I S A P S S P P S A R P      176
481 GGGCGGCTTCCAGTCCCGGTGCATATCCGCCCCAGCTCGCGCGCTTCTGCGCGCGCCT      540

177 C A P W N S W A S S S R R S Q N C A C R      196
541 GCGCCCCCTGCAACTCCTGGGCTTCCAGCTCCCGCGCGCTCCCAAGACTGCGCGTCAGAC      600

197 Q W P Q C A T D P A S W A R D G S G S R      216
601 AATGCCCACAGTGTCCAAGTCAACCTGCGCTCCTGGGCTAGAGATGCGCTCTCGGTCCCGGG      660

217 A G V P A L Q L H L N W G A A G R P G S      236
661 CCGGAGTACCGGCTCTCCAGCTGCATCTGCACTCGCGCGCTGCGAGGTGCTCCCGCGCTGG      720

237 E H T V E G H R F P A E I N V V H L S T      256
721 ACCCAGTGTGGAGGCGCACCGTTTCCCTGCCAGATCCAGGTGCTTCACTCAGCACTG      780

257 A F A R V D E A L G R P G G L A V L A P      276
781 CCTTTCCAGAGTTCAGGAGCCTTCCCGCGCGCGCGGAGGCTGCGCGTGTGCGCGCTT      840

277 F W R R A R K K T V S Y E Q L L S R L E      296
841 TCTCGAGGAGCGCGCGCAAGAAAACAGTGTCTATGACAGTGTCTGTCTCCCTTGGAG      900

297 E I A E E G S E T Q V P G L D I S A L L      316
901 AAATCCCTGAGCAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTCCTCC      960

317 P S D P S R Y F Q Y E G S L T T P P C A      336
961 CCTCTGACTTCAGCGCTACTTCCAAATATGAGCGGTCTCTGACTAGACCGCGCTGTGCC      1020

337 Q G V I W T V F N Q T V N L S A K Q L N      356
1021 AGCGGTGTCATCTGCACTGTGTTTAAACAGACAGTATGCTGAGTGTGAGCAGCTCCACA      1080

357 T L S D T L W G F G D S R L Q L N F R A      376
1081 CCTCTCTGACACCTCTGCGGACCTGCTGACTCTCGGCTACAGCTGAAGTCCGAGCGA      1140

377 T Q P L N G R V I E A S P P A G V D S S      396
1141 CGCAGCCTTTCAATGGGCGAGTGATTGAGGCTCCTTCCCTGCTGAGTGGACAGGAGTC      1200

397 P R A A E P V Q L N S C L A A G D I L A      416
1201 CTCCGCGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGACATCCTAGCCC      1260

417 L V F G L L F A V T S V A P L V Q N R R      436
1261 TCGTTTTTGGCCTCCTTTTTGCTGTGACAGCGTCCCGTTCCCTTGTGCGAGATGAGAGCC      1320

437 Q H R R G T K G G V S V F P S R G S R D      456
1321 ACCACAGAACGGGAACCAAGCGCGGTGTGAGCGTACCGCGCGAGCAGGAGGAGGAGT      1380

457 W S L E A G S W R N *      466
1381 CGACCTTAGAGGCTCGATCTTGGAGAAATGTGAGAAGCCAGCCAGGAGGATCTGAGCGGCA      1440

1441 GCGGTAACCTGCTCCTGCTCCTCATTATCCCACTTCCCTTTAACTGCCAAGAAATTTT      1500

1501 TAAATAAATAATTAAT      1519

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FIG. 15

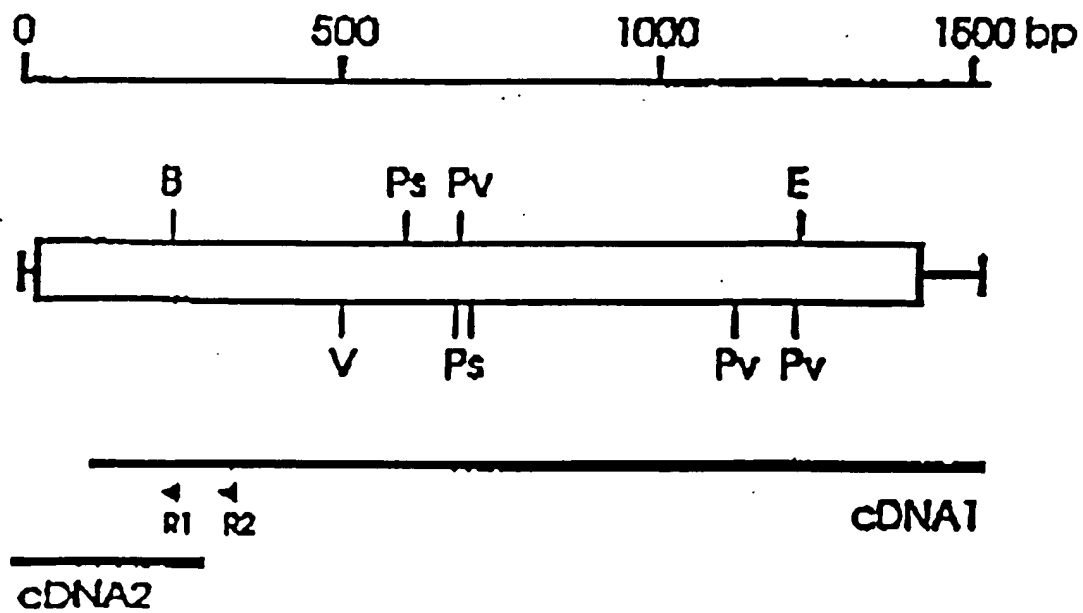


FIG. 16

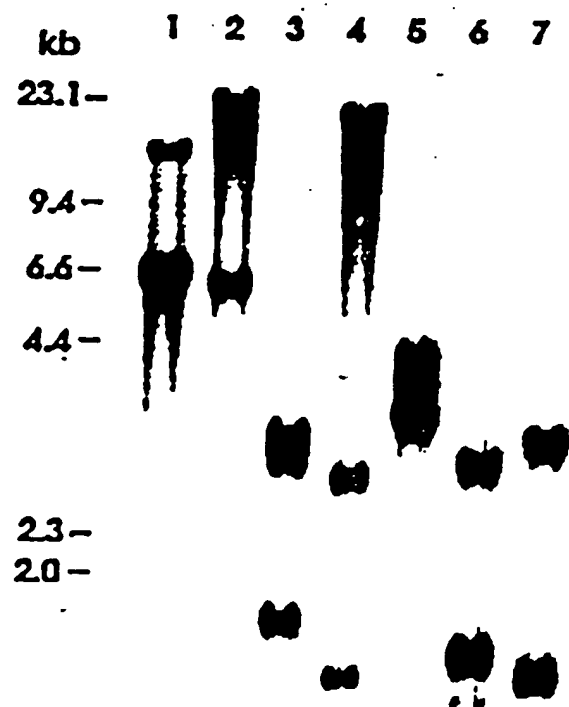


FIG. 17

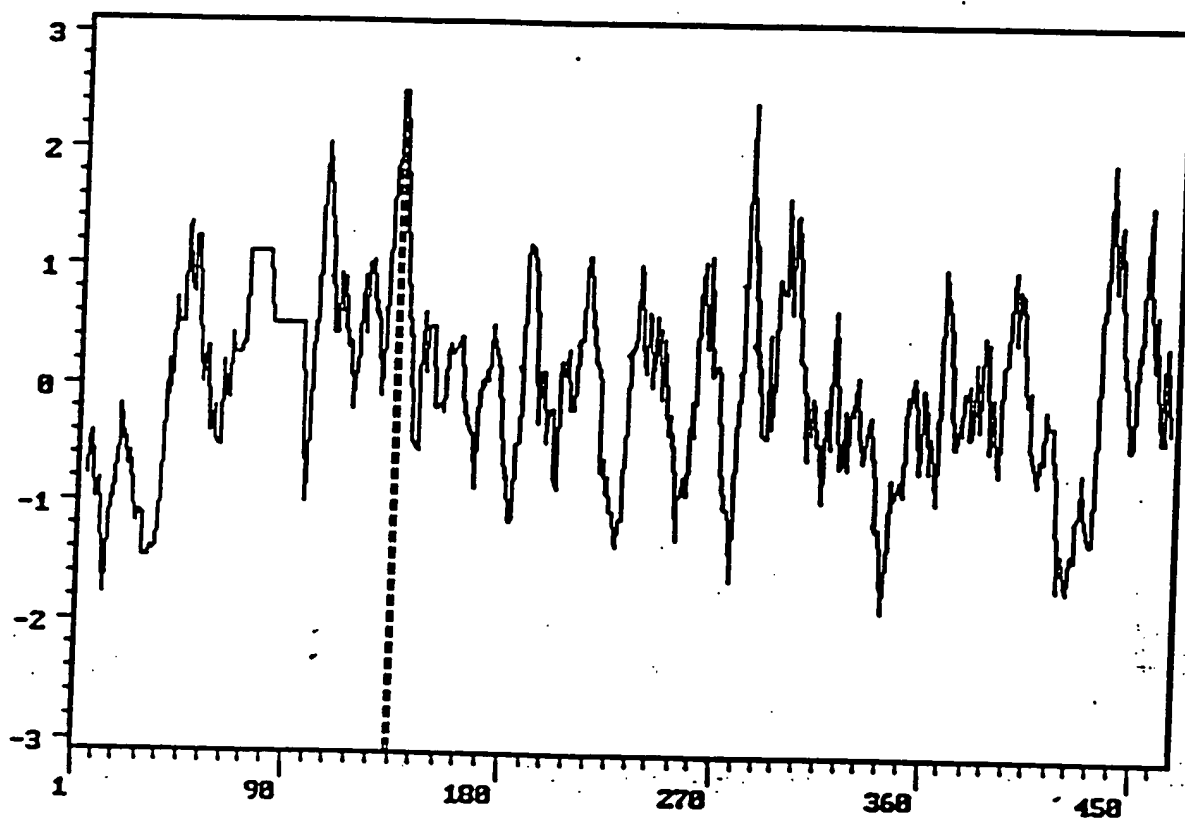


Fig. 18

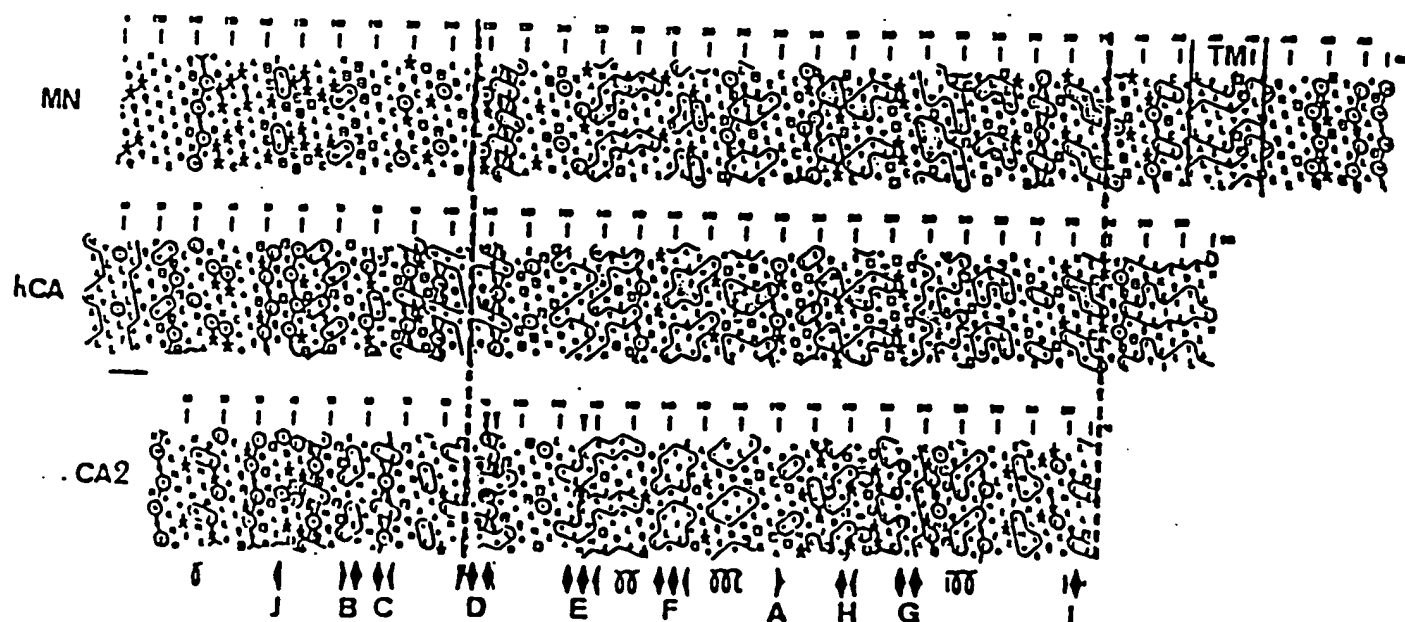


Fig. 19a

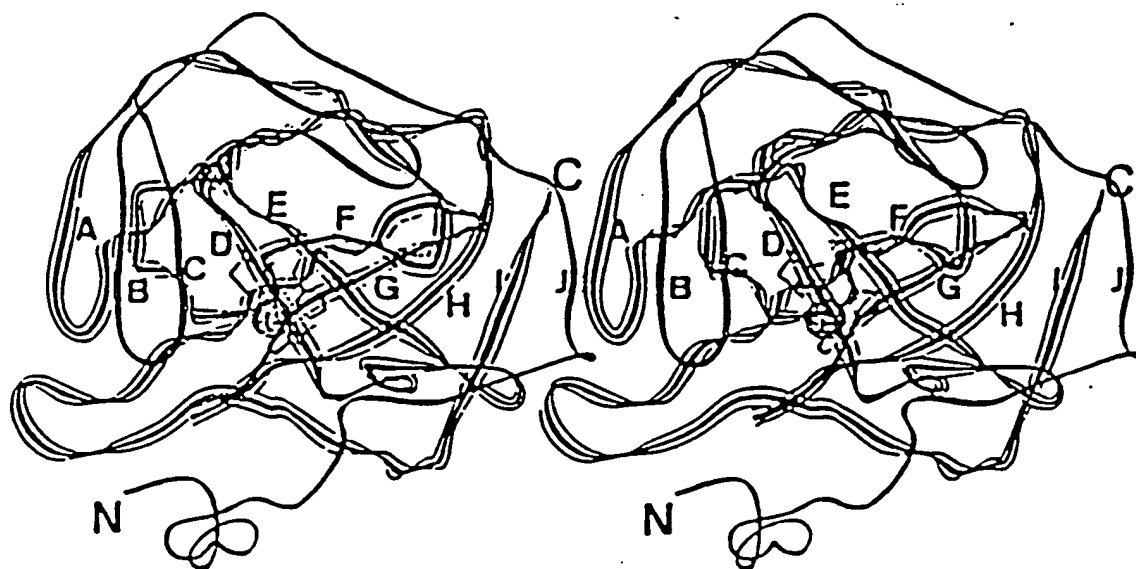


Fig. 19b

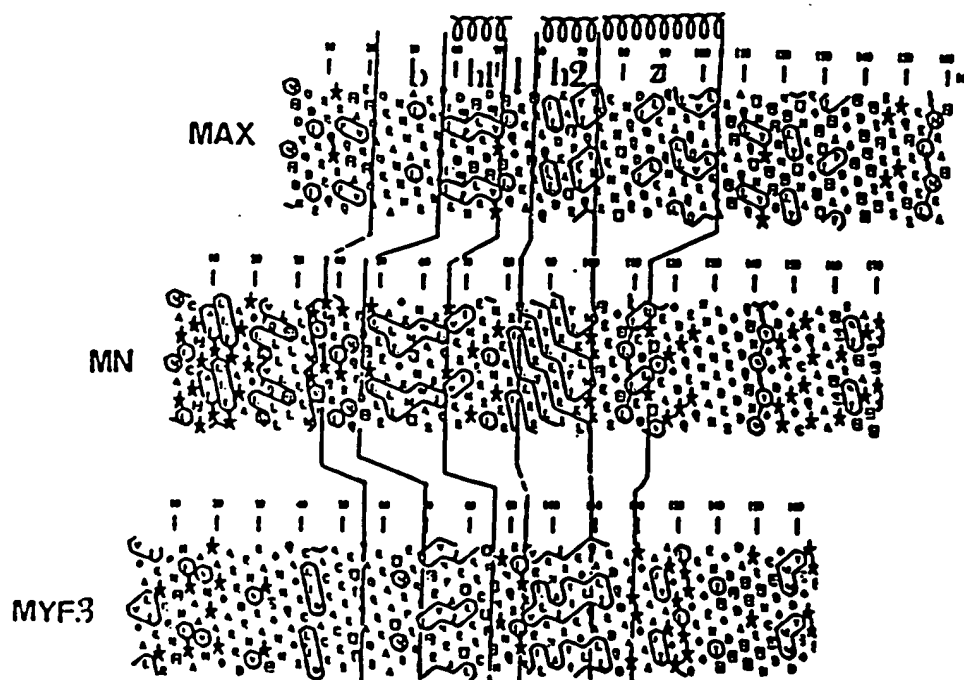


Fig. 19c

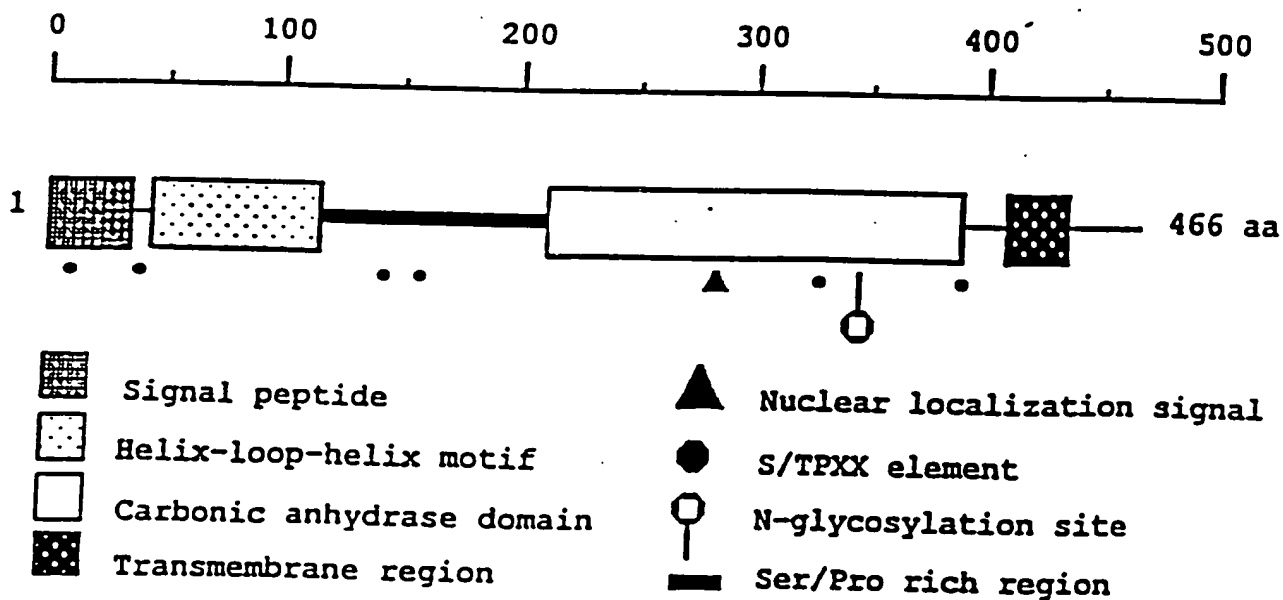


Fig. 19d

# MN Promoter Region

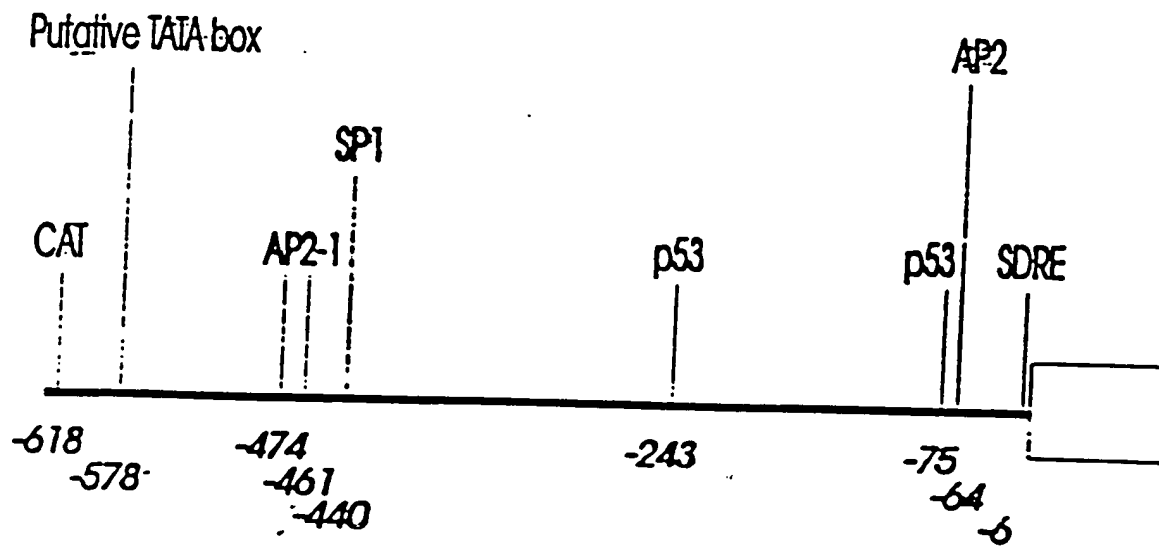


Fig. 20

# 5' MN Genomic Region

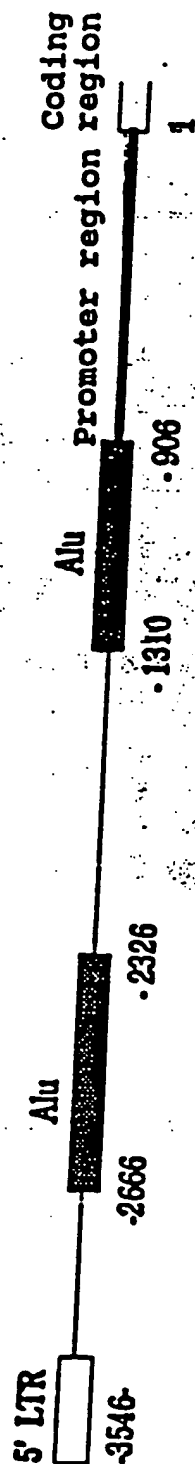


Fig. 21



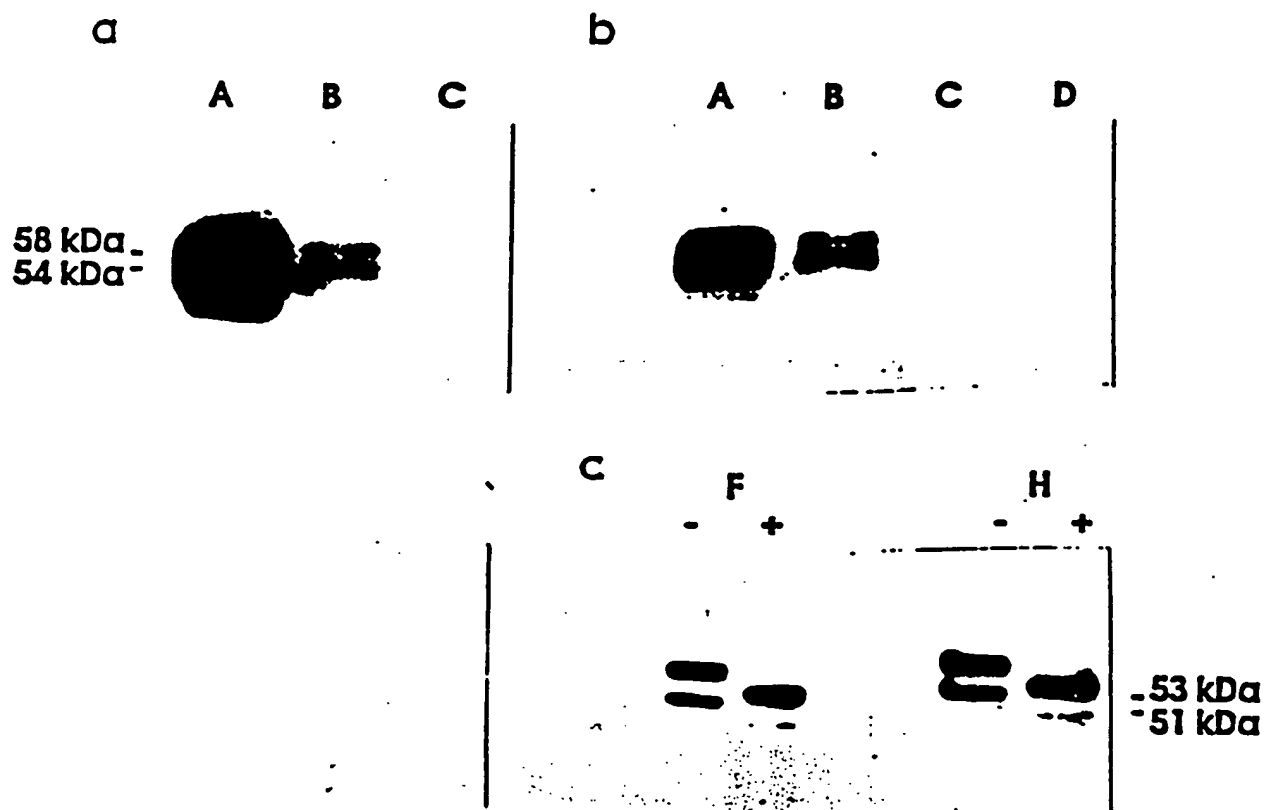


Fig. 22

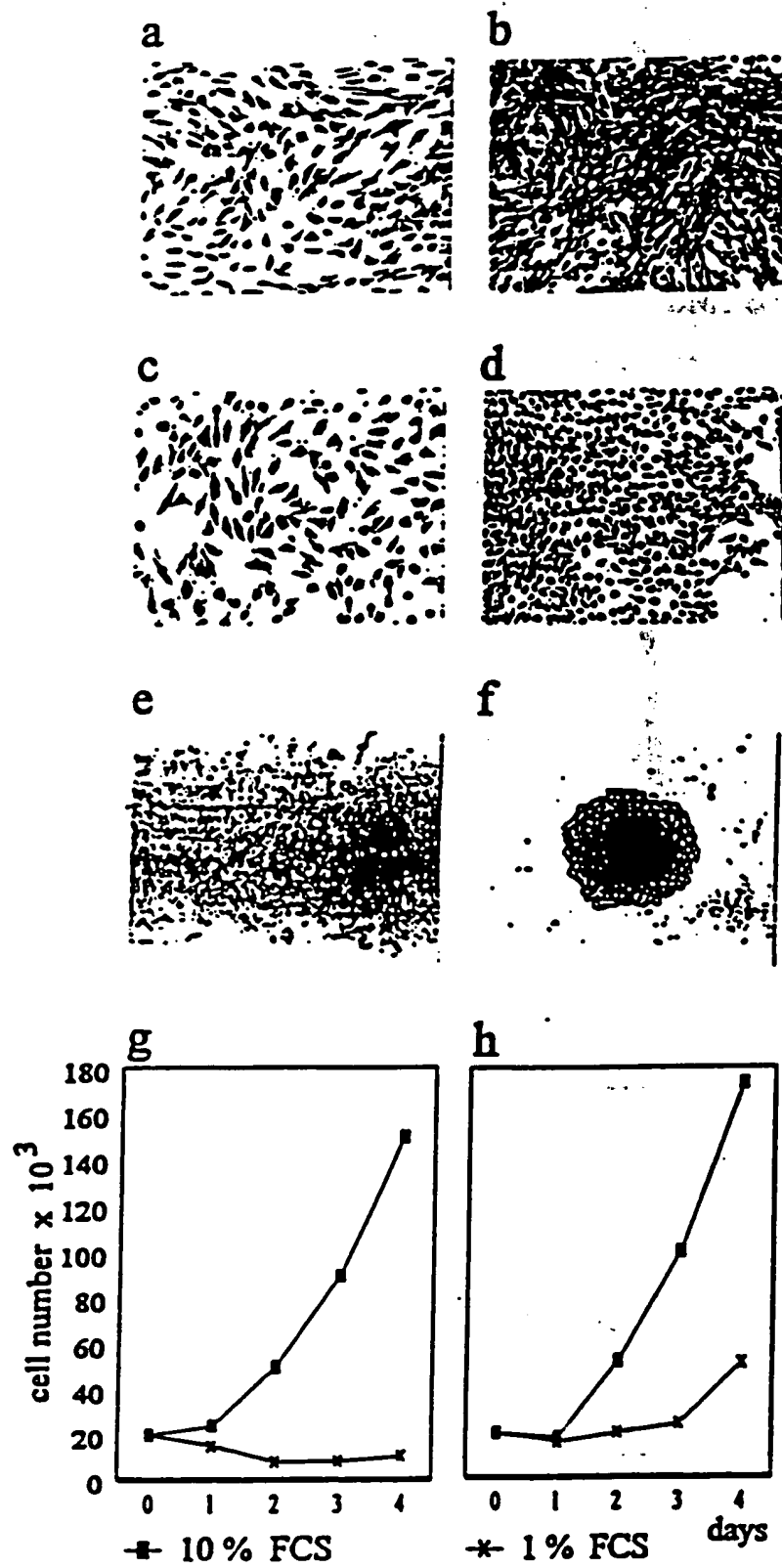
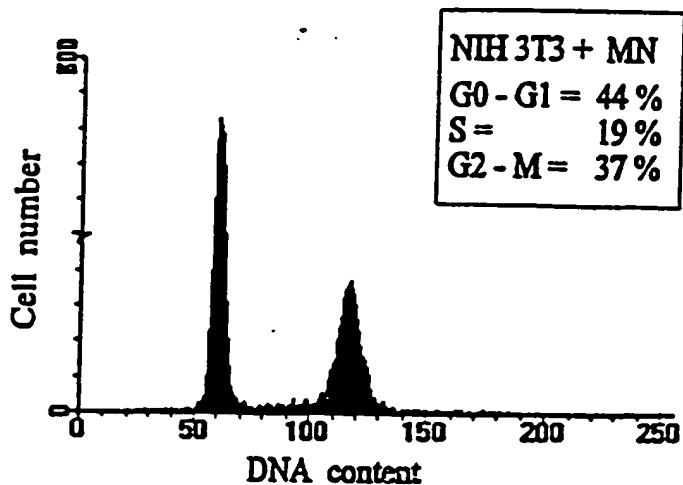
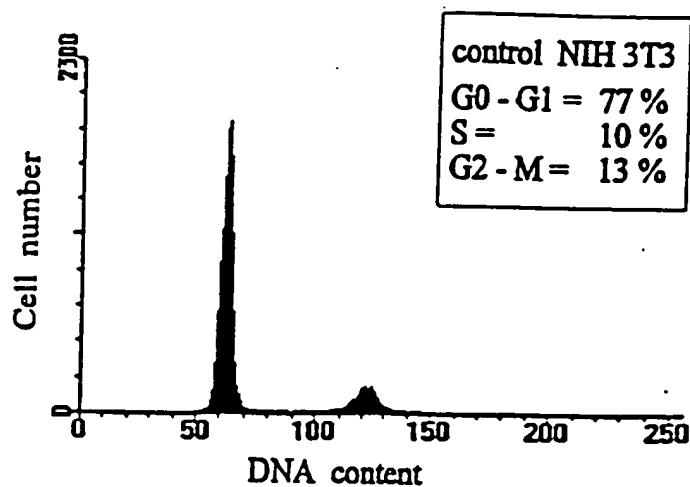
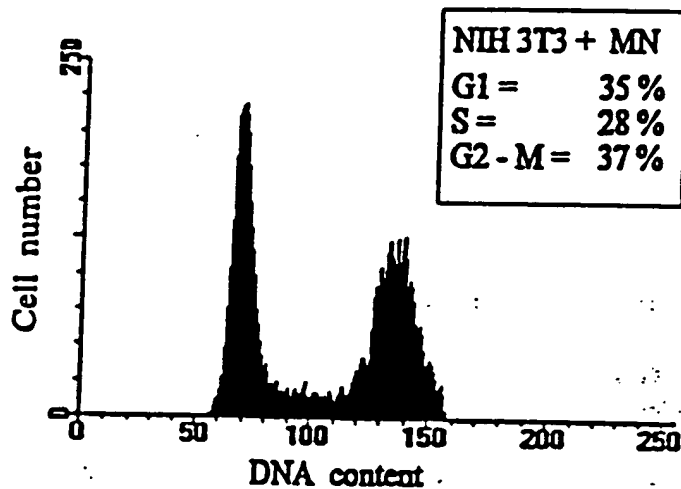
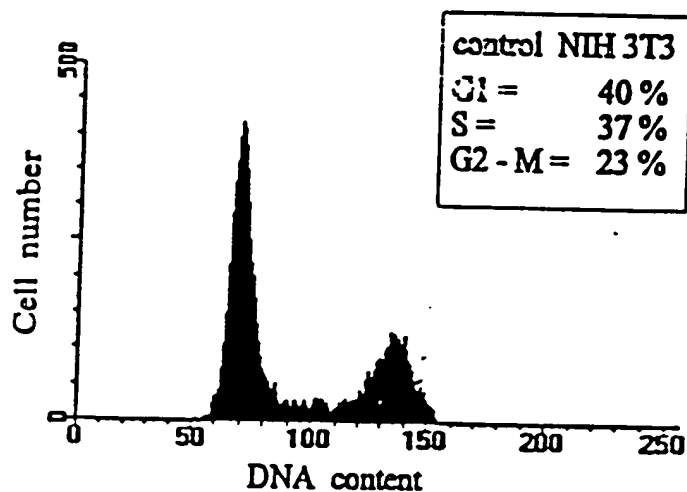


Fig. 23

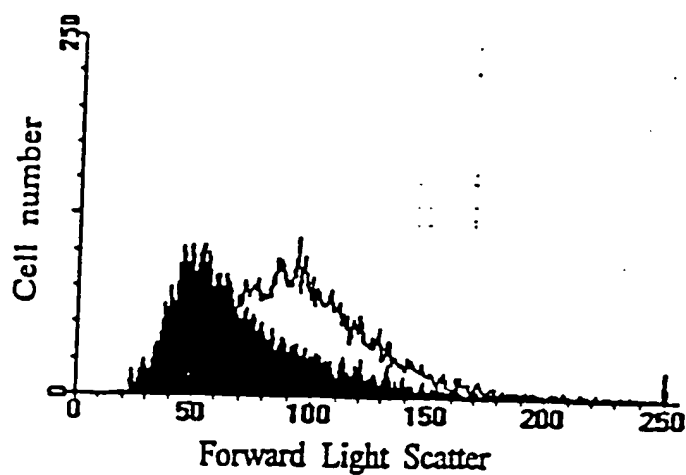
**a**



**b**



**c**



■ NIH 3T3 + MN  
 □ control NIH 3T3

— Kolmogorov-Smirnov Statistics —  
 D/s(n) = 19.03  
 D = 0.36  
 Channel = 70  
 Channels 0 - 255  
 99 % probability of difference

Fig. 24

SQ Sequence 5052 BP; 1201 A; 1249 C; 1201 G; 1399 T.

```
GGATCCTGTT GACTCGTGAC CTTACCCCCA ACCCTGTGCT CTCTGAAACA TGAGCTGTGT
CCACTCAGGG TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG
AAGGCAGCAT GCTCGTTAAG AGTCATCACC AATCCCTAAT CTCAAGTAAT CAGGGACACA
AACACTGCGG AAGGCCGCAG GGTCCCTGTC CTAGGAAAAC CAGAGACCTT TGTTCACTTG
TTTATCTGAC CTTCCCTCCA CTATTGTCCA TGACCCTGCC AAATCCCCCT CTGTGAGAAA
CACCCAAGAA TTATCAATAA AAAAATAAAT TTAACAAAAA AATACAAAAA AAAAAAAAAA
AAAAAAAAAA GACTTACGAA TAGTTATTGA TAAATGAATA GCTATTGGTA AAGCCAAGTA
AATGATCATA TTCAAAACCA GACGGCCATC ATCACAGCTC AAGTCTACCT GATTGTATCT
CTTTATCATT GTCATTCTTT GGATTCACTA GATTAGTCAT CATCCTCAAA ATTCTCCCCC
AAGTTCTAAT TACGTTCCAA ACATTTAGGG GTTACATGAA GCTTGAACCT ACTACCTTCT
TTGCTTTTGA GCCATGAGTT GTAGGAATGA TGAGTTTACA CTTTACATGC TGGGGATTAA
TTTAACTTT ACCTCTAAGT CAGTTGGGTA GCCTTTGGCT TATTTTGTGA GCTAATTTTG
TAGTTAATGG ATGCACTGTG AATCTTGCTA TGATAGTTT CCTCCACACT TTGCCACTAG
GGGTAGGTA GTACTCAGTT TTCAGTAATT GCTTACCTAA GACCCTAAGC CATTTTCTC
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TTTGTGTTGTT TGTTTGTTTG TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TGCCAGGCT
GGAGTAGCAG TGGTGCCATC TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TCACGCCATT
TTCCTGCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGCGC CCGCCACCAT GCCCGCTAA
TTTTTTGTAT TTTTGGTAGA GACGGGGTTT CACCGTGTTA GCCAGAATGG TCTCGATCTC
CTGACTTCGT GATCCACCCG CCTCGGCCTC CCAAAGTTCT GGGATTACAG GTGTGAGCCA
CCGCACCTGG CCAATTTTTT GAGTCTTTTA AAGTAAAAAT ATGTCTTGTA AGCTGGTAAC
TATGGTACAT TTCCTTTTAT TAATGTGGTG CTGACGGTCA TATAGGTTCT TTTGAGTTTG
GCATGCATAT GCTACTTTTT GCAGTCCTTT CATTACATTT TTCTCTCTTC ATTTGAAGAG
CATGTTATAT CTTTTAGCTT CACTTGGCTT AAAAGGTTCT CTCATTAGCC TAACACAGTG
TCATTGTTGG TACCACTTGG ATCATAAGTG GAAAAACAGT CAAGAAATTG CACAGTAATA
CTTGTTTGTA AGAGGGATGA TTCAGGTGAA TCTGACACTA AGAACTCCC CTACCTGAGG
TCTGAGATTC CTC TGACATT GCTGTATATA GGCTTTTCCT TTGACAGCCT GTGACTGCGG
ACTATTTTTT TTAAGCAAGA TAGCTAAAG TTTTGTGAGC CTTTTTCCAG AGAGAGGTCT
CATATCTGCA TCAAGTGAGA ACATATAATG TCTGCATGTT TCCATATTTT AGGAATGTTT
GCTTGTGTTT TATGCTTTTA TATAGACAGG GAACTTGTT CCTCAGTGAC CCAAAGAGG
TGGGAATTGT TATTGGATAT CATCATTGGC CCACGCTTTC TGACCTTGGA AACAAATTAAG
GGTTCATAAT CTCAATTCTG TCAGAATTGG TACAAGAAAT AGCTGCTATG TTTCTTGACA
TTCCACTTGG TAGGAAATAA GAATGTGAAA CTCTTCAGTT GGTGTGTGTC CCTNGTTTTT
TTGCAATTTT CTTCTTACTG TGTTAAAAA AAGTATGATC TTGCTCTGAG AGGTGAGGCA
TTCTTAATCA TGATCTTTAA AGATCAATAA TATAATCCTT TCAAGGATTA TGCTTTTATT
ATAATAAAGA TAATTTGTCT TTAACAGAAT CAATAATATA ATCCCTTAAA GGATTATATC
TTTGCTGGGC GCAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGTGGCC AAGGTGGAAG
GATCAAATTT GCCTACTTCT ATATTATCTT CTAAAGCAGA ATTCATCTCT CTTCCCTCAA
TATGATGATA TTGACAGGGT TTGCCCTCAC TCACTAGATT GTGAGCTCCT GCTCAGGGCA
GGTAGNGTTT TTTGTTTTTG TTTTGTGTTT TCTTTTTTGA GACAGGGTCT TGCTCTGTCA
CCCAGGCCAG AGTGCAATGG TACAGTCTCA GCTCACTGCA GCCTCAACGC CTCGGCTCAA
ACCATCATCC CATTCAGCC TCCTGAGTAG CTGGGACTAC AGGCACATGC CATTACACCT
```

Fig. 25a

GGCTAATTTT TTTGTATTTC TAGTAGAGAC AGGGTTTGGC CATGTTGCCC GGGCTGGTCT  
CGAACTCCTG GACTCAAGCA ATCCACCCAC CTCAGCCTCC CAAAATGAGG GACCGTGTCT  
TATTCATTTC CATGTCCCTA GTCCATAGCC CAGTGCTGGA CCTATGGTAG TACTAAATAA  
ATATTTGTTG AATGCAATAG TAAATAGCAT TTCAGGGAGC AAGAACTAGA TTAACAAAGG  
TGGTAAAAGG TTTGGAGAAA AAAATAATAG TTTAATTTGG CTAGAGTATG AGGGAGAGTA  
GTAGGAGACA AGATGGAAAG GTCTCTTGGG CAAGGTTTTG AAGGAAGTTG GAAGTCAGAA  
GTACACAATG TGATATCGTG GCAGGCAGTG GGGAGCCAAT GAAGGCTTTT GAGCAGGAGA  
GTAATGTGTT GAAAAATAAA TATAGGTTAA ACCTATCAGA GCCCCCTCTGA CACATACACT  
TGCTTTTCAT TCAAGCTCAA GTTGTCTCC CACATACCCA TTACTTAACT CACCCCTCGGG  
CTCCCCTAGC AGCCTGCCCT ACCTCTTTAC CTGCTTCCTG GTGGAGTCAG GGATGTATAC  
ATGAGCTGCT TTCCCTCTCA GCCAGAGACA TGGGGGGCCC CAGCTCCCCCT GCCTTTCCCC  
TTCTGTGCCT GGAGCTGGGA AGCAGGCCAG GGTTAGCTGA GGCTGGCTGG CAAGCAGCTG  
GGTGGTGCCA GGGAGAGCCT GCATAGTGCC AGGTGGTGCC TTGGGTTOCA AGCTAGTCCA  
TGGCCCCGAT AACCTTCTGC CTGTGCACAC ACCTGCCCT CACTCCACCC CCATCCTAGC  
TTTGGTATGG GGGAGAGGGC ACAGGGCCAG ACAAACCTGT GAGACTTTGG CTCCATCTCT  
GCAAAAGGGC GCTCTGTGAG TCAGCCTGCT CCCCCTCAGG CTTGCTCCTC CCCACCCAG  
CTCTCGTTTC CAATGCACGT ACAGCCCCTA CACACCGTGT GCTGGGACAC CCCACAGTCA  
GCGCATGGCT CCCCTGTGCC CCAGCCCCCTG GCTCCTCTG TTGATCCCG CCCCTGCTCC  
AGGCCTCACT GTGCAACTGC TGCTGTCACT GCTGCTTCTG ATGCTGTCC ATCCCCAGAG  
GTTGCCCCGG ATGCAGGAGG ATTCCCCCTT GGAGGAGGCT CTTCTGGGGA AGATGACCCA  
CTGGGCGAGG AGGATCTGCC CAGTGAAGAG GATTACCCA GAGAGGAGGA TCCACCCGGA  
GAGGAGGATC TACCTGGAGA GGAGGATCTA CCTGGAGAGG AGGATCTACC TGAAGTTAAT  
GCCTAAATCA GAAGAAGAGG GCTCCCTGAA GTTAGAGGAT CTACCTACTG TTGAGGCTCC  
TGGAGATCCT CAAGAACCCC AGAATAATGC CCACAGGGAC AAAGAAGGGG ATGACCAGAG  
TCATTGGCGC TATGGAGGCG ACCCGCCTGG CCCCAGGCTG CCGGGGCCGC CGCGGGCCGC  
TTCCAGTCCC CGGTGGATAT CCGCCCCCAG CTCGCGCCT TCTGCCCGGC CCTGCGCCCC  
CTGGAATCC TGGGCTTCCA GCTCCCGCCG CTCCAGAAC TCGCCTGCA GACAATGGCC  
ACAGTGTGCA ACTGACCCCTG CCTCCTGGGC TAGAGATGCC TCTGGGTCCC GGGCGGGAGT  
ACCGGCTCTG CAGCTGCATC TGCATGGGG GGCTGCAGGT CGTCCGGGCT CGGAGCACAC  
TGTGGAAGGC CACCGTTTCC CTGCCGAGAT CCACGTGGTT CACCTCAGCA CCGCCTTTGC  
CAGAGTTGAC GAGGCCTTGG GCGCGCCGGG AGGCCTGGCC GTGTTGGCGC CTTTCTGGAG  
GAGGGCCCCG AAGAAAACAG TGTCTATGA GCAGTTGCTG TCTCGCTTGG AAGAAATCGC  
TGAGGAAGGC TCAGAGACTC AGGTCCCAGG ACTGGACATA TCTGCACTCC TGCCCTCTGA  
CTTCAGCCGC TACTTCCAAT ATGAGGGGTC TCTGACTACA CCGCCCTGTG CCCAGGGTGT  
CATCTGGACT GTGTTTAACC AGACAGTGAT GCTGAGTGCT AAGCAGCTCC ACACCCCTCTC  
TGACACCCTG TGGGGACCTG GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC  
TTTGAATGGG CGAGTGATTG AGGCCTCCTT CCCTGCTGGA GTGGACAGCA GTCTCGGGC  
TGCTGAGCCA GTCCAGCTGA ATTCTGCCT GGCTGCTGGT GACATCCTAG CCCTGGTTTTT  
TGGCCTCCTT TTTGCTGTCA CCAGCGTCGC GTTCCTTGTG CAGATGAGAA GGCAGCACAG  
AAGGGGAACC AAAGGGGGTG TGAGCGTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT  
AGAGGCTGGA TCTTGAGAA TG TGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGTA  
ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA  
AATATTTATA AT

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Fig. 25b